In the Claims:

Please cancel claims 6-10 without prejudice to their presentation in another application. Please amend claims 1 and 17 and add new claims 21-30 as indicated below:

1.   (Amended) A method of identifying a compound which modulates activity of a target RNA comprising

identifying at least one molecular interaction site on said target RNA

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representations of said [target RNA] molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

17.   (Amended) A method of identifying a compound which modulates activity of a target RNA comprising

generating *in silico* a virtual library of compounds predicted or calculated to interact with a molecular interaction site within said RNA;

comparing three dimensional representations of said [target RNA] molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site; and

synthesizing the highly ranked members of said hierarchy of compounds.

-21.   A method of identifying a compound which modulates activity of a target RNA comprising:

identifying at least one molecular interaction site on said target RNA, wherein said target RNA is mRNA, pre-mRNA, tRNA, rRNA, or snRNA;

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generating in silico a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

22. The method of claim 21 further comprising synthesizing the highly ranked members of said hierarchy of compounds.

23. The method of claim 22 further comprising testing said highly ranked members to determine their ability to interact with said molecular interaction site.

24. The method of claim 22 further comprising:

contacting said target RNA with at least one of said highly ranked members to provide a complex between said RNA and the member or members;

ionizing said complex;

fragmenting the ionized complex; and

determining whether highly ranked members binds to the molecular interaction site of said RNA.

25. The method of claim 24 further comprising determining the strength of binding of a highly ranked member in comparison to the binding strength of other highly ranked members.

26. A method of identifying a compound which modulates activity of a target RNA comprising:

identifying at least one molecular interaction site on said target RNA by comparing the nucleotide sequence of said target RNA with the nucleotide sequence of a RNA from a different taxonomic species, identifying at least one conserved region, determining the secondary structure of said conserved region;

generating *in silico* a virtual library of compounds predicted or calculated to interact with said molecular interaction site; and

comparing three dimensional representation of said molecular interaction site with members of the virtual library of compounds to generate a hierarchy of said compounds ranked in accordance with their respective ability to form physical interactions with said molecular interaction site.

27.   The method of claim 26 further comprising synthesizing the highly ranked members of said hierarchy of compounds.

28.   The method of claim 27 further comprising testing said highly ranked members to determine their ability to interact with said molecular interaction site.

29.   The method of claim 27 further comprising

contacting the target RNA with at least one of said highly ranked members to provide a complex between the RNA and the member or members;

ionizing said complex;

fragmenting the ionized complex; and

determining whether highly ranked members binds to the molecular interaction site of said RNA.

30.   The method of claim 29 further comprising determining the strength of binding of a highly ranked member in comparison to the binding strength of other highly ranked members.--

REMARKS

Claims 1-10 and 17-20 are pending in the present application. Claims 6-10 have been canceled without prejudice to their presentation in another application. Claims 1 and 17 have been amended herein. New claims 21-30 have been added herein. Upon entry of the present amendment, claims 1-5 and 17-30 will be pending.